

SEQUENCE LISTING

<110> Booth, Russ
Cahoon, Rebecca E
Hitz, William D
Kinney, Anthony
Yadav, Naren

<120> Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-ACP Desaturase

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<151> 2000-08-22

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<212> DNA

<213> Glycine max

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<212> PRT
<213> Glycine max

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Leu Pro Gln Leu Pro Cys Ser Ser Arg Lys Ala His His Arg His Leu
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Leu Pro Pro Leu Asn Ala Ala Val Ser Ala Ala Pro Phe Lys Ala Arg
      50           55           60

Lys Ala His Ser Met Pro Pro Glu Lys Lys Glu Ile Phe Lys Ser Leu
      65           70           75           80

Glu Gly Trp Ala Ser Glu Trp Val Leu Pro Leu Leu Lys Pro Val Glu
      85           90           95

Gln Cys Trp Gln Pro Gln Asn Phe Leu Pro Asp Pro Ser Leu Pro His
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Glu Glu Phe Ser His Gln Val Lys Glu Leu Arg Glu Arg Thr Lys Glu
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Leu Pro Asp Glu Tyr Phe Val Val Leu Val Gly Asp Met Val Thr Glu
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Asp Ala Leu Pro Thr Tyr Gln Thr Met Ile Asn Asn Leu Asp Gly Val
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Lys Asp Asp Ser Gly Thr Ser Pro Ser Pro Trp Ala Val Trp Thr Arg
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Ala Trp Thr Ala Glu Glu Asn Arg His Gly Asp Leu Leu Arg Thr Tyr
      180          185          190

Leu Tyr Leu Ser Gly Arg Val Asp Met ala Lys Val Glu Lys Thr Val
      195          200          205

His Tyr Leu Ile Ser Ala Gly Met Asp Pro Gly Thr Asp Asn Asn Pro
      210          215          220

Tyr Leu Gly Phe Val Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Val
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Ala His Gly Asn Thr Ala Arg Leu Ala Lys Glu Gly Gly Asp Pro Val
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Leu Ala Arg Leu Cys Gly Thr Ile Ala Ala Asp Glu Lys Arg His Glu
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Asn Ala Tyr Ser Arg Ile Val Glu Lys Leu Leu Glu Val Asp Pro Thr
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Gly Ala Met Val Ala Ile Gly Asn Met Met Glu Lys Lys Ile Thr Met
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Tyr Ser Ala Val Ala Gln Arg Ile Gly Val Tyr Thr Ala Asn Asp Tyr
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Ala Asp Ile Leu Glu Phe Leu Val Glu Arg Trp Arg Leu Glu Lys Leu
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Glu Gly Leu Met ala Glu Gly Lys Arg Ala Gln Asp Phe Val Cys Gly
355 360 365

Leu Ala Pro Arg Ile Arg Arg Leu Gln Glu Arg Ala Asp Glu Arg Ala
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 <213> Zea mays

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 35 40 45
 Cys Arg Ser Ser His Ser Ser Thr Gly Thr Thr Thr Met ala Val Pro
 50 55 60
 Val Leu Lys Arg Arg Glu Lys Gln Asp Glu Xaa Gln Glu Trp Met Gly
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 Tyr Leu Ala Pro Glu Lys Leu Glu Val Leu Ala His Leu Glu Pro Trp
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 Ala Glu Ala His Val Leu Pro Leu Leu Lys Pro Ala Glu Glu
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 <212> PRT
 <213> Zea mays

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Thr Gln Ala Pro Ala Arg Arg Arg Gln Cys Arg Val Ser Ala Ala Ala
      20        25        30

Val Gly Ala Pro Ala Ala Arg Ala Arg Val Thr His Ser Met Pro Pro
      35        40        45

Glu Lys Ala Glu Val Phe Arg Ser Leu Glu Gly Trp Ala Ala Arg Ser
      50        55        60

Leu Leu Pro Leu Leu Lys Pro Val Glu Glu Cys Trp Gln Pro Ala Asp
      65        70        75        80

Phe Leu Pro Asp Ser Ser Ser Glu Met Phe Gly His Glu Val Arg Glu
      85        90        95

Leu Arg Ala Arg Ala Ala Gly Leu Pro Asp Glu Tyr Phe Val Val Leu
      100       105       110

Val Gly Asp Met Val Thr Glu Glu Ala Leu Pro Thr Tyr Gln Thr Met
      115       120       125

Ile Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser Asn Cys
      130       135       140

Pro Trp Ala Val Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His
      145       150       155       160

Gly Asp Ile Leu Gly Lys Tyr Met Tyr Leu Ser Gly Arg Val Asp Met
      165       170       175

Arg Met Val Glu Lys Thr Val Gln Tyr Leu Ile Gly Ser Gly Met Asp
      180       185       190

Pro Gly Thr Glu Asn Asn Pro Tyr Leu Gly Phe Val Tyr Thr Ser Phe
      195       200       205

Gln Glu Arg Ala Thr Ala Val Ser His Gly Asn Thr Ala Arg Leu Pro
      210       215       220

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Arg Ala His Gly Asp Asp Phe Leu Ala Arg Ala Cys Gly Thr Asn Arg
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Val
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 <213> Oryza sativa

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 35 40 45

His Gly Asn Thr Ala Arg Leu Val Gly Ala Arg Gly His Gly Asp Ala
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Ala Leu Ala Arg Val Cys Gly Thr Val Ala Ala Asp Glu Lys Arg His
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Glu Ala Ala Tyr Thr Arg Ile Val Ser Arg Leu Leu Glu Ala Asp Pro
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Asp Ala Gly Val Arg Ala Val Ala Arg Met Leu Arg Arg Gly Val
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 <213> Zea mays

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Cys	Arg	Ser	Ser	His	Ser	Ser	Thr	Gly	Thr	Thr	Thr	Met	Ala	Val	Pro
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Ala	Glu	Ala	His	Val	Leu	Pro	Leu	Leu	Lys	Pro	Ala	Glu	Glu	Ala	Trp
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Gln	Pro	Ser	Asp	Met	Leu	Pro	Asp	Pro	Ala	Ala	Leu	Gly	Asp	Glu	Gly
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Phe	His	Asp	Ala	Cys	Arg	Glu	Leu	Arg	Ala	Arg	Ala	Ala	Ser	Val	Pro
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	210					215					220				
Leu	Ile	Ala	Ser	Gly	Met	Ala	Met	Asn	Ala	Ala	Arg	Ser	Pro	Tyr	His
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Gly	Phe	Ile	Tyr	Val	Ala	Phe	Gln	Glu	Arg	Ala	Thr	Ala	Ile	Ser	His
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Gly	Asn	Met	Ala	Arg	His	Val	Gly	Ala	His	Gly	Asp	His	Val	Leu	Ala
			260				265							270	

Arg Val Cys Gly Ala Ile Met Ala Asp Glu Lys Arg His Glu Thr Ala
275 280 285

Tyr Thr Arg Ile Val Ala Lys Leu Phe Glu Val Asp Pro Asp Ala Ala
290 295 300

Val Arg Ala Leu Gly Tyr Met Met Arg His Arg Ile Thr Met Pro Ala
305 310 315 320

Ala Leu Met Thr Asp Gly Arg Asp Ala His Leu Tyr Ala His Tyr Ala
325 330 335

Ala Ala Ala Gln Gln Thr Gly Val Tyr Thr Ala Ser Asp Tyr Arg Ser
340 345 350

Ile Leu Glu His Leu Ile Arg Gln Trp Arg Val Glu Glu Leu Ala Ala
355 360 365

Gly Leu Ser Gly Glu Gly Arg Arg Ala Arg Asp Tyr Val Cys Gly Leu
370 375 380

Pro His Lys Ile Arg Arg Met Glu Glu Lys Ala His Asp Arg Ala Ala
385 390 395 400

Gln Thr Gln Lys Lys Pro Thr Ser Val Pro Phe Ser Trp Ile Phe Asp
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Arg Ser Val Asn Val Val Ile Pro
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<213> Zea mays

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<400> 12

Met Gln Ala His Gly Ile Ala Ile Arg Ala Arg Gly Pro Val Ala Ala
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Thr Gln Ala Pro Ala Arg Arg Arg Gln Cys Arg Val Ser Ala Ala Ala
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Val Gly Ala Pro Ala Ala Arg Ala Arg Val Thr His Ser Met Pro Pro
35 40 45

Glu Lys Ala Glu Val Phe Arg Ser Leu Glu Gly Trp Ala Ala Arg Ser
50 55 60

Leu Leu Pro Leu Leu Lys Pro Val Glu Glu Cys Trp Gln Pro Ala Asp
65 70 75 80

Phe Leu Pro Asp Ser Ser Ser Glu Met Phe Gly His Glu Val Arg Glu
85 90 95

Leu Arg Ala Arg Ala Ala Gly Leu Pro Asp Glu Tyr Phe Val Val Leu
100 105 110

Val Gly Asp Met Val Thr Glu Glu Ala Leu Pro Thr Tyr Gln Thr Met
115 120 125

Ile Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser Asn Cys
130 135 140

Pro Trp Ala Val Trp Thr Arg Ala Trp Thr Ala Glu Asn Arg His
145 150 155 160

Gly Asp Ile Leu Gly Lys Tyr Met Tyr Leu Ser Gly Arg Val Asp Met
165 170 175

Arg Met Val Glu Lys Thr Val Gln Tyr Leu Ile Gly Ser Gly Met Asp
180 185 190

Pro Gly Thr Glu Asn Asn Pro Tyr Leu Gly Phe Val Tyr Thr Ser Phe
195 200 205

Gln Glu Arg Ala Thr Ala Val Ser His Gly Asn Thr Ala Arg Leu Ala
210 215 220

Arg Ala His Gly Asp Asp Val Leu Ala Arg Ala Cys Gly Thr Ile Ala
225 230 235 240

Ala Asp Glu Lys Arg His Glu Thr Ala Tyr Gly Arg Ile Val Glu Gln
245 250 255

Leu Leu Gln Leu Asp Pro Glu Gly Ala Val Leu Ala Val Ala Asp Met
260 265 270

Met Arg Lys Arg Ile Thr Met Pro Ala His Leu Met His Asp Gly Arg
 275 280 285

Asp Met Asp Leu Phe Glu His Phe Ala Ala Val Ala Gln Arg Leu Gly
 290 295 300

Val Tyr Thr Ala Arg Asp Tyr Ala Asp Ile Val Glu Phe Leu Val Lys
 305 310 315 320

Arg Trp Lys Leu Glu Thr Leu Glu Ser Gly Leu Ser Gly Glu Gly Arg
 325 330 335

Arg Ala Arg Asp Phe Val Cys Gly Leu Ala Pro Arg Met Arg Arg Ala
 340 345 350

Ala Glu Arg Ala Glu Asp Arg Ala Lys Lys Asp Glu Pro Arg Met Val
 355 360 365

Lys Phe Ser Trp Ile Phe Asp Arg Glu Ala Val Val
 370 375 380

<210> 13
 <211> 773
 <212> DNA
 <213> *Oryza sativa*

<400> 13
 gcaccaggta cctctccggc cgtctcgaca tggcccgagg ggagcgcgcc gtgcaccgcc 60
 tcctccgctc cggcatggcc gtccgaccgc cgtgcagccc gtaccacgcc ttctgtctaca 120
 cggcggttcca ggagcgcgcc acggcgggtcg cccacggcaa caccgcgcgg ctggtcggcg 180
 cgcgagggca cggcgacgcc gccctcgccc gcgtctcggg caccgtcgcc gccgacgaga 240
 agcggcacga ggccgcctac acccgcatcg tctccaggct cctcgaggcc gaccgggacg 300
 ccggcggtgc cgcggtggcg cgcattgctac ggccaggggg cgcattgccc acctcgcccc 360
 tctccgacgg ccgcgcgcac gacctctacg cctgcgtcgt gtccctcgcc gaggcggcgg 420
 ggacgtacac ggtgtcggac taactgtcca tcgtcgagca cctggtgcgg gaggcggcgg 480
 tggaggagct cgcggcgggg ctctccggcg aaggcgcggc cgcgcgggac tacgtgtgcg 540
 agctcccgca gaagatccgg aggatgaagg agaagggcca tgagaggcgg gtcaaggccc 600
 agaagaagcc catcagcatc ccgattaatt ggatatttga taggcacgtc agtgcctatgc 660
 tgccctaatt taattaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 720
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 773

<210> 14
 <211> 219
 <212> PRT
 <213> *Oryza sativa*

<400> 14
 Tyr Leu Ser Gly Arg Phe Asp Met Ala Glu Val Glu Arg Ala Val His
 1 5 10 15

Arg Leu Ile Arg Ser Gly Met Ala Val Asp Pro Pro Cys Ser Pro Tyr
 20 25 30

His Ala Phe Val Tyr Thr Ala Phe Gln Glu Arg Ala Thr Ala Val Ala
 35 40 45

His Gly Asn Thr Ala Arg Leu Val Gly Ala Arg Gly His Gly Asp Ala
50 55 60

Ala Leu Ala Arg Val Cys Gly Thr Val Ala Ala Asp Glu Lys Arg His
65 70 75 80

Glu Ala Ala Tyr Thr Arg Ile Val Ser Arg Leu Leu Glu Ala Asp Pro
85 90 95

Asp Ala Gly Val Arg Ala Val Ala Arg Met Leu Arg Arg Gly Val Ala
100 105 110

Met Pro Thr Ser Pro Ile Ser Asp Gly Arg Arg Asp Asp Leu Tyr Ala
115 120 125

Cys Val Val Ser Leu Ala Glu Gln Ala Gly Thr Tyr Thr Val Ser Asp
130 135 140

Tyr Cys Ser Ile Val Glu His Leu Val Arg Glu Trp Arg Val Glu Glu
145 150 155 160

Leu Ala Ala Gly Leu Ser Gly Glu Gly Arg Ala Arg Asp Tyr Val
165 170 175

Cys Glu Leu Pro Gln Lys Ile Arg Arg Met Lys Glu Lys Ala His Glu
180 185 190

Arg Ala Val Lys Ala Gln Lys Lys Pro Ile Ser Ile Pro Ile Asn Trp
195 200 205

Ile Phe Asp Arg His Val Ser Val Met Leu Pro
210 215

<210> 15

<211> 1318

<212> DNA

<213> *Oryza sativa*

<400> 15

gcacgagaac tagctactgt agttgactga cagtgaatgt ggcagtcattg caggtcgttg 60
gaaccgtgcg tgtcagtgcc tcgcgcgcgg tggtggcgcc ctgcgcgcgg cagtcgcgcg 120
tgtcccgccg ggtgctgacg gccgcgcgga cggcgacggc gacgcggcgc cgcgtgacgc 180
actcgatgcc gcgcgagaag gcggagggtgt tccggtcgct ggaagggttg gcgagggtcg 240
cgctgctgcc gctgctcaag cccgtggagg agtgcgtgca gccgacggac ttctgcgcgg 300
actcgtcgct ggagatgttc gagcaccagg tcacacgact ccgcgcgcgc gccgcggggc 360
tcgccgacga tactctcgte gtgctggtcg gggacatgat tacgcaggag gcgctgccga 420
cgtaccagac catgatcaac acgctcgacg gcgtccgcga cgagaccggc gccagcgccct 480
gcgccatggc cctctggacg cgcacctgga ccgcgcgagg gaaccgccac ggcgacatcc 540
tcggcaagta catgtacctc tcgcgcgcgg tcgacatgag catggtcgag aagacgctcc 600
agtaacctcat cggctccggc atggatccgg ggacggagaa caaccgtac ctgggggttcg 660
tgtaccacag cttccaggag ccgcgcgacg ccgtgtgcga cgggaacacg gcgcgcctcg 720
ccagggcgca cggggacgac gtccctggcg gccactgcgg caccatgcgc gccgacgaga 780
agcggcagca agcggcgtag gggcgcatcg tggagcagct gctgcggctc gccccggacg 840
gcgcgatgct cgccatgcgc gacatgatgc acaagcggat caccatgcgc gcgcacctca 900
tgacacagcg ccgcgacatg aacctgttgc accacttcgc cgcgctggcg cgcgacctca 960
acgtatacac ccgcgcgcgac tacgccgaca tcgtcgagtt cctcgtaacg cgggtggaagc 1020
tggagaccct ggagactggg ctctccggcg agggccggag ggcccgggac ttctgtgctg 1080
ggctcgcgaa gaggatgcgg cgggccgcgg agcgggctga ggacaggcct aagaaggatg 1140
agcagagga ggtcaagttc agctggatct atgataggga agtgattgtc tagtttaact 1200

tgtcttgggt gaattctgaa ttcccagtc tagatgatca tgccatttcg ttatcatctc 1260
 tgttcttctg ttctctttgc aatgcagtaa attggaata aaaaaaaaaa aaaaaaaa 1318

<210> 16
 <211> 381
 <212> PRT
 <213> *Oryza sativa*

<400> 16
 Met Gln Val Val Gly Thr Val Arg Val Ser Gly Cys Gly Ala Val Val
 1 5 10 15
 Ala Pro Ser Arg Arg Gln Cys Arg Val Ser Ala Ala Val Leu Thr Ala
 20 25 30
 Ala Glu Thr Ala Thr Ala Thr Arg Arg Arg Val Thr His Ser Met Pro
 35 40 45
 Pro Glu Lys Ala Glu Val Phe Arg Ser Leu Glu Gly Trp Ala Arg Ser
 50 55 60
 Ser Leu Leu Pro Leu Leu Lys Pro Val Glu Glu Cys Trp Gln Pro Thr
 65 70 75 80
 Asp Phe Leu Pro Asp Ser Ser Ser Glu Met Phe Glu His Gln Val His
 85 90 95
 Glu Leu Arg Ala Arg Ala Ala Gly Leu Pro Asp Glu Tyr Phe Val Val
 100 105 110
 Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Gln Thr
 115 120 125
 Met Ile Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser Ala
 130 135 140
 Cys Pro Trp Ala Val Trp Thr Arg Thr Trp Thr Ala Glu Glu Asn Arg
 145 150 155 160
 His Gly Asp Ile Leu Gly Lys Tyr Met Tyr Leu Ser Gly Arg Val Asp
 165 170 175
 Met Arg Met Val Glu Lys Thr Val Gln Tyr Leu Ile Gly Ser Gly Met
 180 185 190
 Asp Pro Gly Thr Glu Asn Asn Pro Tyr Leu Gly Phe Val Tyr Thr Ser
 195 200 205
 Phe Gln Glu Arg Ala Thr Ala Val Ser His Gly Asn Thr Ala Arg Leu
 210 215 220
 Ala Arg Ala His Gly Asp Asp Val Leu Ala Arg Thr Cys Gly Thr Ile
 225 230 235 240
 Ala Ala Asp Glu Lys Arg His Glu Thr Ala Tyr Gly Arg Ile Val Glu
 245 250 255
 Gln Leu Leu Arg Leu Asp Pro Asp Gly Ala Met Leu Ala Ile Ala Asp
 260 265 270

Met Met His Lys Arg Ile Thr Met Pro Ala His Leu Met His Asp Gly
 275 280 285
 Arg Asp Met Asn Leu Phe Asp His Phe Ala Ala Val Ala Gln Arg Leu
 290 295 300
 Asn Val Tyr Thr Ala Arg Asp Tyr Ala Asp Ile Val Glu Phe Leu Val
 305 310 315 320
 Lys Arg Trp Lys Leu Glu Thr Leu Glu Thr Gly Leu Ser Gly Glu Leu
 325 330 335
 Arg Arg Ala Arg Asp Phe Val Cys Gly Leu Ala Lys Arg Met Arg Arg
 340 345 350
 Ala Ala Glu Arg Ala Glu Asp Arg Ala Lys Lys Asp Glu Gln Arg Lys
 355 360 365
 Val Lys Phe Ser Trp Ile Tyr Asp Arg Glu Val Ile Val
 370 375 380
 <210> 17
 <211> 384
 <212> PRT
 <213> *Lupinus luteus*
 <400> 17
 Met Gln Ile Gln Thr Cys Tyr Ser Ile Arg Ile Gln Ile Leu Pro Leu
 1 5 10 15
 Pro Trp Ala Arg Thr Gly Arg His Lys Met Leu Pro Pro Ile Ala
 20 25 30
 Ala Ile Ser Ala Thr Pro Pro Ser Leu Lys Ser Pro Lys Thr His Ser
 35 40 45
 Met Pro Pro Glu Lys Ile Glu Ile Phe Lys Ser Leu Glu Ser Trp Ala
 50 55 60
 Ser Gln Ser Val Leu Pro Leu Leu Lys Pro Val Glu Gln Cys Trp Gln
 65 70 75 80
 Pro Gln Glu Phe Val Pro Asp Ser Ser Leu Pro Phe Gly Asp Phe Thr
 85 90 95
 Asp Gln Val Lys Ala Leu Arg Asp Arg Thr Ala Glu Leu Pro Glu Glu
 100 105 110
 Tyr Phe Val Val Leu Val Gly Asp Met Ile Thr Glu Asp Ala Leu Pro
 115 120 125
 Thr Tyr Gln Ser Met Ile Asn Asn Leu Asp Gly Val Arg Asp Glu Thr
 130 135 140
 Gly Ser Ser Pro Ser Pro Trp Ala Leu Trp Thr Arg Ala Trp Thr Ala
 145 150 155 160

Glu Glu Lys Arg His Gly Asp Leu Leu Arg Thr Tyr Leu Tyr Leu Ser
 165 170 175
 Gly Arg Val Asp Met Lys Lys Ile Glu Lys Thr Val Gln Tyr Leu Ile
 180 185 190
 Gly Ser Gly Met Asp Pro Gly Thr Glu Asn Asn Pro Tyr Leu Gly Phe
 195 200 205
 Val Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Val Ser His Gly Asn
 210 215 220
 Thr Ala Arg Leu Ala Lys Glu Gly Gly Asp Pro Val Leu Ala Arg Ile
 225 230 235 240
 Cys Gly Thr Ile Ala Ala Asp Glu Lys Arg His Glu Asn Ala Tyr Ser
 245 250 255
 Arg Ile Val Glu Lys Leu Leu Glu Leu Asp Pro Thr Gly Ala Met Val
 260 265 270
 Ala Ile Gly Asp Met Met Gln Lys Lys Ile Thr Met Pro Ala His Leu
 275 280 285
 Met Tyr Asp Gly Glu Asp Pro Lys Leu Phe Asp His Phe Ser Ala Val
 290 295 300
 Ala Gln Arg Met Gly Val Tyr Thr Ala Asn Asp Tyr Ala Asp Ile Leu
 305 310 315 320
 Glu Phe Leu Ile Gly Arg Trp Arg Leu Glu Lys Val Gln Asp Leu Lys
 325 330 335
 Asp Glu Gly Lys Lys Ala Gln Asp Phe Val Cys Gly Leu Ala Pro Arg
 340 345 350
 Ile Arg Arg Leu Gln Glu Arg Ala Asp Glu Arg Ala Arg Lys Met Lys
 355 360 365
 Pro His Ala Val Lys Phe Ser Trp Ile Phe Asn Lys Glu Ile Ile Leu
 370 375 380

<210> 18
 <211> 396
 <212> PRT
 <213> Cucumis sativus

<400> 18
 Met Ala Leu Lys Phe His Pro Leu Thr Ser Gln Ser Pro Lys Leu Pro
 1 5 10 15
 Ser Phe Arg Met Pro Gln Leu Ala Ser Leu Arg Ser Pro Lys Phe Val
 20 25 30
 Met Ala Ser Thr Leu Arg Ser Thr Ser Arg Glu Val Glu Thr Leu Lys
 35 40 45
 Lys Pro Phe Met Pro Pro Arg Glu Val His Leu Gln Val Thr His Ser
 50 55 60

Met Pro Pro Gln Lys Met Glu Ile Phe Lys Ser Leu Glu Asp Trp Ala
 65 70 75 80
 Glu Glu Asn Leu Leu Val His Leu Lys Pro Val Glu Arg Cys Trp Gln
 85 90 95
 Pro Gln Asp Phe Leu Pro Asp Ser Ala Phe Glu Gly Phe His Glu Gln
 100 105 110
 Val Arg Glu Leu Arg Glu Arg Ala Lys Glu Leu Pro Asp Glu Tyr Phe
 115 120 125
 Val Val Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr
 130 135 140
 Gln Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala
 145 150 155 160
 Ser Pro Thr Pro Trp Ala Ile Trp Thr Arg Ala Trp Thr Ala Glu Glu
 165 170 175
 Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg
 180 185 190
 Val Asp Met Arg Gln Val Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser
 195 200 205
 Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe Ile Tyr
 210 215 220
 Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala
 225 230 235 240
 Arg Leu Ala Lys Glu His Gly Asp Ile Lys Leu Ala Gln Ile Cys Gly
 245 250 255
 Thr Ile Thr Ala Asp Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile
 260 265 270
 Val Glu Lys Leu Phe Glu Ile Asp Pro Glu Gly Thr Val Ile Ala Phe
 275 280 285
 Glu Glu Met Met Arg Lys Lys Val Ser Met Pro Ala His Leu Met Tyr
 290 295 300
 Asp Gly Arg Asp Asp Asn Leu Phe His His Phe Ser Ala Val Ala Gln
 305 310 315 320
 Arg Leu Gly Val Tyr Thr Ala Lys Asp Tyr Ala Asp Ile Leu Glu Phe
 325 330 335
 Leu Val Gly Arg Trp Lys Val Glu Ser Leu Thr Gly Leu Ser Gly Glu
 340 345 350
 Gly Gln Lys Ala Gln Asp Tyr Val Cys Ala Leu Pro Ala Arg Ile Arg
 355 360 365
 Lys Leu Glu Glu Arg Ala Gln Gly Arg Ala Lys Glu Gly Pro Thr Ile
 370 375 380

Pro Phe Ser Trp Ile Phe Asp Arg Gln Val Lys Leu
385 390 395

<210> 19

<211> 374

<212> PRT

<213> Arabidopsis thaliana

<400> 19

Met Pro Ser Pro Ser Thr Phe Leu Ala Ser Arg Pro Arg Gly Pro Ala
1 5 10 15

Lys Ile Ser Ala Val Ala Ala Pro Val Arg Pro Ala Leu Lys His Gln
20 25 30

Asn Lys Ile His Thr Met Pro Pro Glu Lys Met Glu Ile Phe Lys Ser
35 40 45

Leu Asp Gly Trp Ala Lys Asp Gln Ile Leu Pro Leu Leu Lys Pro Val
50 55 60

Asp Gln Cys Trp Gln Pro Ala Ser Phe Leu Pro Asp Pro Ala Leu Pro
65 70 75 80

Phe Ser Glu Phe Thr Asp Gln Val Arg Glu Leu Arg Glu Arg Thr Ala
85 90 95

Ser Leu Pro Asp Glu Tyr Phe Val Val Leu Val Gly Asp Met Ile Thr
100 105 110

Glu Asp Ala Leu Pro Thr Tyr Gln Thr Met Ile Asn Thr Leu Asp Gly
115 120 125

Val Arg Asp Glu Thr Gly Ala Ser Glu Ser Ala Trp Ala Ser Trp Thr
130 135 140

Arg Ala Trp Thr Ala Glu Asn Arg His Gly Asp Leu Leu Arg Thr
145 150 155 160

Tyr Leu Tyr Leu Ser Gly Arg Val Asp Met Leu Met Val Glu Arg Thr
165 170 175

Val Gln His Leu Ile Gly Ser Gly Met Asp Pro Gly Thr Glu Asn Asn
180 185 190

Pro Tyr Leu Gly Phe Val Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe
195 200 205

Val Ser His Gly Asn Thr Ala Arg Leu Ala Lys Ser Ala Gly Asp Pro
210 215 220

Val Leu Ala Arg Ile Cys Gly Thr Ile Ala Ala Asp Glu Lys Arg His
225 230 235 240

Glu Asn Ala Tyr Val Arg Ile Val Glu Lys Leu Leu Glu Ile Asp Pro
245 250 255

Asn Gly Ala Val Ser Ala Val Ala Asp Met Met Arg Lys Lys Ile Thr
 260 265 270
 Met Pro Ala His Leu Met Thr Asp Gly Arg Asp Pro Met Leu Phe Glu
 275 280 285
 His Phe Ser Ala Val Ala Gln Arg Leu Glu Val Tyr Thr Ala Asp Asp
 290 295 300
 Tyr Ala Asp Ile Leu Glu Phe Leu Val Gly Arg Trp Arg Leu Glu Lys
 305 310 315 320
 Leu Glu Gly Leu Thr Gly Glu Gly Gln Arg Ala Gln Glu Phe Val Cys
 325 330 335
 Gly Leu Ala Gln Arg Ile Arg Arg Leu Gln Glu Arg Ala Asp Glu Arg
 340 345 350
 Ala Lys Lys Leu Lys Lys Thr His Glu Val Cys Phe Ser Trp Ile Phe
 355 360 365
 Asp Lys Gln Ile Ser Val
 370
 <210> 20
 <211> 398
 <212> PRT
 <213> Simmondsia chinensis
 <400> 20
 Met Ala Leu Lys Leu His His Thr Ala Phe Asn Pro Ser Met Ala Val
 1 5 10 15
 Thr Ser Ser Gly Leu Pro Arg Ser Tyr His Leu Arg Ser His Arg Val
 20 25 30
 Phe Met Ala Ser Ser Thr Ile Gly Ile Thr Ser Lys Glu Ile Pro Asn
 35 40 45
 Ala Lys Lys Pro His Met Pro Pro Arg Glu Ala His Val Gln Lys Thr
 50 55 60
 His Ser Met Pro Pro Gln Lys Ile Glu Ile Phe Lys Ser Leu Glu Gly
 65 70 75 80
 Trp Ala Glu Glu Asn Val Leu Val His Leu Lys Pro Val Glu Lys Cys
 85 90 95
 Trp Gln Pro Gln Asp Phe Leu Pro Asp Pro Ala Ser Glu Gly Phe Met
 100 105 110
 Asp Gln Val Lys Glu Leu Arg Glu Arg Thr Lys Glu Ile Pro Asp Glu
 115 120 125
 Tyr Leu Val Val Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro
 130 135 140
 Thr Tyr Gln Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr
 145 150 155 160

Gly Ala Ser Leu Thr Ser Trp Ala Ile Trp Thr Arg Ala Trp Thr Ala
 165 170 175
 Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Leu Tyr Leu Thr
 180 185 190
 Gly Arg Val Asp Met Lys Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile
 195 200 205
 Gly Ser Gly Met Asp Pro Arg Ser Glu Asn Asn Pro Tyr Leu Gly Phe
 210 215 220
 Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn
 225 230 235 240
 Thr Ala Arg Leu Ala Lys Asp His Gly Asp Phe Gln Leu Ala Gln Val
 245 250 255
 Cys Gly Ile Ile Ala Ala Asp Glu Lys Arg His Glu Thr Ala Tyr Thr
 260 265 270
 Lys Ile Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Ala Val Leu
 275 280 285
 Ala Leu Ala Asp Met Met Arg Lys Lys Val Ser Met Pro Ala His Leu
 290 295 300
 Met Tyr Asp Gly Lys Asp Asp Asn Leu Phe Glu Asn Tyr Ser Ala Val
 305 310 315 320
 Ala Gln Gln Ile Gly Val Tyr Thr Ala Lys Asp Tyr Ala Asp Ile Leu
 325 330 335
 Glu His Leu Val Asn Arg Trp Lys Val Glu Asn Leu Met Gly Leu Ser
 340 345 350
 Gly Glu Gly His Lys Ala Gln Asp Phe Val Cys Gly Leu Ala Pro Arg
 355 360 365
 Ile Arg Lys Leu Gly Glu Arg Ala Gln Ser Leu Ser Lys Pro Val Ser
 370 375 380
 Leu Val Pro Phe Ser Trp Ile Phe Asn Lys Glu Leu Lys Val
 385 390 395

<210> 21

<211> 411

<212> PRT

<213> *Arabidopsis thaliana*

<400> 21

Met Ala Leu Leu Leu Asn Ser Thr Ile Thr Val Ala Met Lys Gln Asn
 1 5 10 15

Pro Leu Val Ala Val Ser Phe Pro Arg Thr Thr Cys Leu Gly Ser Ser
 20 25 30

Phe Ser Pro Pro Arg Leu Leu Arg Val Ser Cys Val Ala Thr Asn Pro
35 40 45
Ser Lys Thr Ser Glu Glu Thr Asp Lys Lys Lys Phe Arg Pro Ile Lys
50 55 60
Glu Val Pro Asn Gln Val Thr His Thr Ile Thr Gln Glu Lys Leu Glu
65 70 75 80
Ile Phe Lys Ser Met Glu Asn Trp Ala Gln Glu Asn Leu Leu Ser Tyr
85 90 95
Leu Lys Pro Val Glu Ala Ser Trp Gln Pro Gln Asp Phe Leu Pro Glu
100 105 110
Thr Asn Asp Glu Asp Arg Phe Tyr Glu Gln Val Lys Glu Leu Arg Asp
115 120 125
Arg Thr Lys Glu Ile Pro Asp Asp Tyr Phe Val Val Leu Val Gly Asp
130 135 140
Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Gln Thr Thr Leu Asn Thr
145 150 155 160
Leu Asp Gly Val Lys Asp Glu Thr Gly Gly Ser Leu Thr Pro Trp Ala
165 170 175
Val Trp Val Arg Ala Trp Thr Ala Glu Glu Asn Arg His Gly Asp Leu
180 185 190
Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg Val Asp Met Arg His Val
195 200 205
Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp Ser Lys Phe
210 215 220
Glu Asn Asn Pro Tyr Asn Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg
225 230 235 240
Ala Thr Phe Ile Ser His Gly Asn Thr Ala Lys Leu Ala Thr Thr Tyr
245 250 255
Gly Asp Thr Thr Leu Ala Lys Ile Cys Gly Thr Ile Ala Ala Asp Glu
260 265 270
Lys Arg His Glu Thr Ala Tyr Thr Arg Ile Val Glu Lys Leu Phe Glu
275 280 285
Ile Asp Pro Asp Gly Thr Val Gln Ala Leu Ala Ser Met Met Arg Lys
290 295 300
Arg Ile Thr Met Pro Ala His Leu Met His Asp Gly Arg Asp Asp Asp
305 310 315 320
Leu Phe Asp His Tyr Ala Ala Val Ala Gln Arg Ile Gly Val Tyr Thr
325 330 335
Ala Thr Asp Tyr Ala Gly Ile Leu Glu Phe Leu Leu Arg Arg Trp Glu
340 345 350

Val Glu Lys Leu Gly Met Gly Leu Ser Gly Glu Gly Arg Arg Ala Gln
355 360 365

Asp Tyr Leu Cys Thr Leu Pro Gln Arg Ile Arg Arg Leu Glu Glu Arg
370 375 380

Ala Asn Asp Arg Val Lys Leu Ala Ser Lys Ser Lys Pro Ser Val Ser
385 390 395 400

Phe Ser Trp Ile Tyr Gly Arg Glu Val Glu Leu
405 410

<210> 22

<211> 396

<212> PRT

<213> Linum usitatissimum

<400> 22

Met Ala Leu Lys Leu Asn Pro Val Thr Thr Phe Pro Ser Thr Arg Ser
1 5 10 15

Leu Asn Asn Phe Ser Ser Arg Ser Pro Arg Thr Phe Leu Met Ala Ala
20 25 30

Ser Thr Phe Asn Ser Thr Ser Thr Lys Glu Ala Glu Lys Leu Lys Lys
35 40 45

Ser His Gly Pro Pro Lys Glu Val His Met Gln Val Thr His Ser Met
50 55 60

Pro Pro Gln Lys Leu Glu Ile Phe Lys Ser Leu Glu Gly Trp Ala Glu
65 70 75 80

Asp Val Leu Leu Pro His Leu Lys Pro Val Glu Lys Cys Trp Gln Pro
85 90 95

Gln Asp Phe Leu Pro Glu Pro Glu Ser Asp Gly Phe Glu Glu Gln Val
100 105 110

Lys Glu Leu Arg Ala Arg Ala Lys Glu Leu Pro Asp Asp Tyr Phe Val
115 120 125

Val Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Gln
130 135 140

Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser
145 150 155 160

Leu Thr Pro Trp Ala Ile Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn
165 170 175

Arg His Gly Asp Leu Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg Val
180 185 190

Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly
195 200 205

Met Asp Pro Lys Thr Glu Asn Asn Pro Tyr Leu Gly Phe Ile Tyr Thr
210 215 220

Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala Arg
 225 230 235 240
 Leu Ala Lys Asp His Gly Asp Met Lys Leu Ala Gln Ile Cys Gly Ile
 245 250 255
 Ile Ala Ala Asp Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val
 260 265 270
 Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr Val Leu Ala Leu Ala
 275 280 285
 Asp Met Met Arg Lys Lys Ile Ser Met Pro Ala His Leu Met Tyr Asp
 290 295 300
 Gly Glu Asp Asp Asn Leu Phe Asp Asn Tyr Ser Ser Val Ala Gln Arg
 305 310 315
 Ile Gly Val Tyr Thr Ala Lys Asp Tyr Ala Asp Ile Leu Glu Phe Leu
 325 330 335
 Val Gly Arg Trp Lys Val Asp Ala Phe Thr Gly Leu Ser Gly Glu Gly
 340 345 350
 Asn Lys Ala Gln Asp Phe Val Cys Gly Leu Pro Ala Arg Ile Arg Lys
 355 360 365
 Leu Glu Glu Arg Ala Ala Gly Arg Ala Lys Gln Thr Ser Lys Ser Val
 370 375 380
 Pro Phe Ser Trp Ile Phe Ser Arg Glu Leu Val Leu
 385 390 395

<210> 23
 <211> 391
 <212> PRT
 <213> Glycine max

<400> 23
 Met ala Leu Arg Leu Asn Pro Ile Pro Thr Gln Thr Phe Ser Leu Pro
 1 5 10 15
 Gln Met Pro Ser Leu Arg Ser Pro Arg Phe Arg Met ala Ser Thr Leu
 20 25 30
 Arg Ser Gly Ser Lys Glu Val Glu Asn Ile Lys Lys Pro Phe Thr Pro
 35 40 45
 Pro Arg Glu Val His Val Gln Val Thr His Ser Met Pro Pro Gln Lys
 50 55 60
 Ile Glu Ile Phe Lys Ser Leu Glu Asp Trp Ala Asp Gln Asn Ile Leu
 65 70 75 80
 Thr His Leu Lys Pro Val Glu Lys Cys Trp Gln Pro Gln Asp Phe Leu
 85 90 95

Pro Asp Pro Ser Ser Asp Gly Phe Glu Glu Gln Val Lys Glu Leu Arg
 100 105 110
 Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Val Leu Val Gly
 115 120 125
 Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Gln Thr Met Leu Asn
 130 135 140
 Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser Leu Thr Ser Trp
 145 150 155 160
 Ala Ile Trp Thr Arg Ala Trp Thr Ala Glu Asn Arg His Gly Asp
 165 170 175
 Leu Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg Val Asp Met Lys Gln
 180 185 190
 Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp Pro Arg
 195 200 205
 Thr Glu Asn Ser Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe Gln Glu
 210 215 220
 Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala Arg Leu Ala Lys Glu
 225 230 235 240
 His Gly Asp Ile Lys Leu Ala Gln Ile Cys Gly Met Ile Ala Ser Asp
 245 250 255
 Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Phe
 260 265 270
 Glu Val Asp Pro Asp Gly Thr Val Met ala Phe Ala Asp Met Met Arg
 275 280 285
 Lys Lys Ile Ala Met Pro Ala His Leu Met Tyr Asp Gly Arg Asp Asp
 290 295 300
 Asn Leu Phe Asp Asn Tyr Ser Ala Val Ala Gln Arg Ile Gly Val Tyr
 305 310 315 320
 Thr Ala Lys Asp Tyr Ala Asp Ile Leu Glu Phe Leu Val Gly Arg Trp
 325 330 335
 Lys Val Glu Gln Leu Thr Gly Leu Ser Gly Glu Gly Arg Lys Ala Gln
 340 345 350
 Glu Tyr Val Cys Gly Leu Pro Pro Arg Ile Arg Arg Leu Glu Glu Arg
 355 360 365
 Ala Gln Ala Arg Gly Lys Glu Ser Ser Thr Leu Lys Phe Ser Trp Ile
 370 375 380
 His Asp Arg Glu Val Leu Leu
 385 390

<210> 24
 <211> 80

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: ELVISLIVES complementary
region of pKS106 and pKS124

<400> 24
cggccggagc tggctcatctc gctcatcgtc gagtcggcgg ccgccgactc gacgatgagc 60
gagatgacca gctccggcgg                                     80

<210> 25
<211> 154
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: ELVISLIVES complementary
region of pKS133

<400> 25
cgccggcgagc tggctcatctc gctcatcgtc gagtcggcgg ccggagctgg tcatctcgct 60
catcgtcgag tcggcggcgg ccgactcgac gatgagcgag atgaccagct ccggcggcgg 120
actcgacgat gaggcgagatg accagctcgc gccg                                     154

<210> 26
<211> 6611
<212> DNA
<213> Plasmid pBS68

<220>
<221> Unsure
<222> (4436)..(4436)
<223> n = A, C, G, or T

<400> 26
cgcgccctatg cgggaccatc gcagcggacg agaagcggca cgagaacgcg tactcaagaa 60
tcgtggagaa gcttctggaa gtggacccca ccggggcgaat ggtggccata gggaacatga 120
tgagagaaga gatcacgatg ccggcgccacc ttatgtacga tggggatgac ccagagctat 180
tcgaqcacta ctccgctgtg gcgcagcgca taggcgtgta caccgccaac gactacgcag 240
acatcttggg tttctcgttg acggtgaaga ttggagaagc ttgaaggatt gatgcctgag 300
gggaagcggg cccagagatt tccgtgtgtg ggttgcoccc gaggattagg aggttccaag 360
aacgcgctga tgagcgagcg cgttaagatga agaagcatca tgcggttaag ttcagttgga 420
tttcaataaa agaattgcct tttgtgagcg ccgcgaactc gacgatgagc gagatgacca 480
gctccggcgg ccgactcgac gatgagcgag atgaccagct ccggccgcga cacaagtgtg 540
agagtactaa ataaatgctt tggttgtacg aaatcattac actaaataaa ataataaag 600
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